

GFAT-anglais

SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> GLUTAMINE:FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE (GFAT) COMPRISING AN INTERNAL PURIFICATION TAG, AND ITS USE FOR THE SCREENING OF COMPOUNDS

<130> WOB 03 BP CNR GFAT

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 2046

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2046)

<223>

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<221> misc_feature

<222> (170)..(170)

<223> t ou c

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cga	gaa	atc	ctg	gag	acc	cta	atc	aaa	ggc	ctt	cag	aga	ctg	gag	tac	96
Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
			20					25					30			

aga	gga	tat	gat	tct	gct	ggt	gtg	gga	ttt	gat	gga	ggc	aat	gat	aaa	144
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys	
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gat	tgg	gaa	gcc	aat	gcc	tgc	aaa	anc	cag	ctt	att	aag	aag	aaa	gga	192
Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly	
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aaa	ggt	aag	gca	ctg	gat	gaa	gaa	ggt	cac	aag	caa	caa	gat	atg	gat	240
Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp	
65					70				75					80		

ttg	gat	ata	gaa	ttt	gat	gta	cac	ctt	gga	ata	gct	cat	acc	cgt	tgg	288
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp	
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gca	aca	cat	gga	gaa	ccc	agt	cct	gtc	aat	agc	cac	ccc	cag	cgc	tct	336
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	
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gat	aaa	aat	aat	gaa	ttt	atc	ggt	att	cac	aat	gga	atc	atc	acc	aac	384
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GFAT-anglais															
Asp	Lys	Asn 115	Asn	Glu	Phe	Ile	Val 120	Ile	His	Asn	Gly	Ile 125	Ile	Thr	Asn
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tct Ser 145	gaa Glu	aca Thr	gac Asp	aca Thr	gag Glu 150	aca Thr	att Ile	gcc Ala	aag Lys	ctc Leu 155	ggt Val	aag Lys	tat Tyr	atg Met	tat Tyr 160
gac Asp	aat Asn	cgg Arg	gaa Glu	agt Ser 165	caa Gln	gat Asp	acc Thr	agc Ser	ttt Phe 170	act Thr	acc Thr	ttg Leu	gtg Val	gag Glu 175	aga Arg
ggt Val	atc Ile	caa Gln 180	caa Gln	ttg Leu	gaa Glu	ggt Gly	gct Ala	ttt Phe 185	gca Ala	ctt Leu	gtg Val	ttt Phe 190	aaa Lys	agt Ser	gtt Val
cat His	ttt Phe	ccc Pro 195	ggg Gly	caa Gln	gca Ala	gtt Val	ggc Gly 200	aca Thr	agg Arg	cga Arg	ggt Gly	agc Ser 205	cct Pro	ctg Leu	ttg Leu
att Ile	ggt Gly 210	gta Val	cgg Arg	agt Ser	gaa Glu	cat His 215	aaa Lys	ctt Leu	tct Ser	act Thr	gat Asp 220	cac His	att Ile	cct Pro	ata Ile
ctc Leu 225	tac Tyr	aga Arg	aca Thr	ggc Gly	aaa Lys 230	gac Asp	aag Lys	aaa Lys	gga Gly	agc Ser 235	tgc Cys	aat Asn	ctc Leu	tct Ser	cgt Arg 240
gtg Val	gac Asp	agc Ser	aca Thr	acc Thr 245	tgc Cys	ctt Leu	ttc Phe	ccg Pro	gtg Val 250	gaa Glu	gaa Glu	aaa Lys	gca Ala	gtg Val 255	gag Glu
tat Tyr	tac Tyr	ttt Phe 260	gct Ala	tct Ser	gat Asp	gca Ala	agt Ser	gct Ala 265	gtc Val	ata Ile	gaa Glu	cac His	acc Thr 270	aat Asn	cgc Arg
gtc Val	atc Ile	ttt Phe 275	ctg Leu	gaa Glu	gat Asp	gat Asp 280	gtt Val	gca Ala	gca Ala	gta Val	gtg Val 285	gat Asp	gga Gly	cgt Arg	
ctt Leu 290	tct Ser	atc Ile	cat His	cga Arg	att Ile	aaa Lys 295	cga Arg	act Thr	gca Ala	gga Gly	gat Asp 300	cac His	ccc Pro	gga Gly	cga Arg
gct Ala 305	gtg Val	caa Gln	aca Thr	ctc Leu	cag Gln 310	atg Met	gaa Glu	ctc Leu	cag Gln	cag Gln 315	atc Ile	atg Met	aag Lys	ggc Gly	aac Asn 320
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gtg Val	aac Asn	aca Thr	atg Met 340	aga Arg	gga Gly	aga Arg	gtc Val	aac Asn 345	ttt Phe	gat Asp	gac Asp	tat Tyr	act Thr 350	gtg Val	aat Asn
ttg Leu	ggt Gly	ggt Gly	ttg Leu	aag Lys	gat Asp	cac His	ata Ile	aag Lys	gag Glu	atc Ile	cag Gln	aga Arg	tgc Cys	cgg Arg	cgt Arg

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ttg	att	ctt	att	gct	tgt	gga	aca	agt	tac	cat	gct	ggt	gta	gca	aca			1152
Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	Ser	Tyr	His	Ala	Gly	Val	Ala	Thr			
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cgt	caa	ggt	ctt	gag	gag	ctg	act	gag	ttg	cct	gtg	atg	gtg	gaa	cta			1200
Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu	Pro	Val	Met	Val	Glu	Leu			
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gca	agt	gac	ttc	ctg	gac	aga	aac	aca	cca	gtc	ttt	cga	gat	gat	ggt			1248
Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro	Val	Phe	Arg	Asp	Asp	Val			
				405					410					415				
tgc	ttt	ttc	ctt	agt	caa	tca	ggt	gag	aca	gca	gat	act	ttg	atg	ggt			1296
Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Thr	Leu	Met	Gly			
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ctt	cgt	tac	tgt	aag	gag	aga	gga	gct	tta	act	gtg	ggg	atc	aca	aac			1344
Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	Ala	Leu	Thr	Val	Gly	Ile	Thr	Asn			
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aca	ggt	ggc	agt	tcc	ata	tca	cgg	gag	aca	gat	tgt	gga	ggt	cat	att			1392
Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	Asp	Cys	Gly	Val	His	Ile			
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aat	gct	ggt	cct	gag	att	ggt	gtg	gcc	agt	aca	aag	gct	tat	acc	agc			1440
Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser			
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Gln	Phe	Val	Ser	Leu	Val	Met	Phe	Ala	Leu	Met	Met	Cys	Asp	Asp	Arg			
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atc	tcc	atg	caa	gaa	aga	cgc	aaa	gag	atc	atg	ctt	gga	ttg	aaa	cgg			1536
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Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val	Leu	Ser	Met	Asp	Asp	Glu	Ile	Gln			
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aaa	cta	gca	aca	gaa	ctt	tat	cat	cag	aag	tca	ggt	ctg	ata	atg	gga			1632
Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	Gln	Lys	Ser	Val	Leu	Ile	Met	Gly			
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Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys			
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Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile	Leu	Ala	Gly	Glu	Leu	Lys			
				565					570					575				
cat	ggc	cct	ctg	gct	ttg	gtg	gat	aaa	ttg	atg	cct	gtg	atc	atg	atc			1776
His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	Met	Pro	Val	Ile	Met	Ile			
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Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys	Gln	Asn	Ala	Leu	Gln	Gln			
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gtg	gtt	gct	cgg	cag	ggg	cgg	cct	gtg	gta	att	tgt	gat	aag	gag	gat	1872
Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	Val	Val	Ile	Cys	Asp	Lys	Glu	Asp	
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act	gag	acc	att	aag	aac	aca	aaa	aga	acg	atc	aag	gtg	ccc	cac	tca	1920
Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	Arg	Thr	Ile	Lys	Val	Pro	His	Ser	
625					630					635					640	
gtg	gac	tgc	ttg	cag	ggc	att	ctc	agc	gtg	atc	cct	tta	cag	ttg	ctg	1968
Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	Ile	Pro	Leu	Gln	Leu	Leu	
				645					650					655		
gct	ttc	cac	ctt	gct	gtg	ctg	aga	ggc	tat	gat	gtt	gat	ttc	cca	cgg	2016
Ala	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	Asp	Val	Asp	Phe	Pro	Arg	
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 35 40 45
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
 50 55 60
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
 65 70 75 80
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp
 85 90 95
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser
 100 105 110
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn
 115 120 125
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu
 130 135 140
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr
 145 150 155 160

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Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg
 165 170 175
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val
 180 185 190
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu
 195 200 205
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile
 210 215 220
 Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg
 225 230 235 240
 Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu
 245 250 255
 Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg
 260 265 270
 Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg
 275 280 285
 Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro Gly Arg
 290 295 300
 Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys Gly Asn
 305 310 315 320
 Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu Ser Val
 325 330 335
 Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr Val Asn
 340 345 350
 Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys Arg Arg
 355 360 365
 Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val Ala Thr
 370 375 380
 Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu Leu
 385 390 395 400
 Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp Val
 405 410 415
 Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Met Gly
 420 425 430
 Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile Thr Asn
 435 440 445
 Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val His Ile
 450 455 460
 Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser
 465 470 475 480
 Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp Asp Arg

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490

485

495

Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu Lys Arg
500 505 510
Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu Ile Gln
515 520 525
Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile Met Gly
530 535 540
Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys Ile Lys
545 550 555 560
Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu Leu Lys
565 570 575
His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile Met Ile
580 585 590
Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu Gln Gln
595 600 605
Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys Glu Asp
610 615 620
Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro His Ser
625 630 635 640
Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu Leu
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Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr
20 25 30
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Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu
35 40 45
gtc aaa gaa aga cac att cag ctg gtc aag aaa agg ggg aaa gtc aag 192

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65					70					75					80
gag	ttt	gag	aca	cac	ttc	ggc	att	gcc	cac	acg	cgc	tgg	gcc	acc	cac
Glu	Phe	Glu	Thr	His	Phe	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His
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ggg	gtc	ccc	agt	gct	gtc	aac	agc	cac	cct	cag	cgc	tca	gac	aaa	ggc
Gly	Val	Pro	Ser	Ala	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	Asp	Lys	Gly
			100					105					110		
aac	gaa	ttt	gtt	gtc	atc	cac	aat	ggg	atc	atc	aca	aat	tac	aaa	gat
Asn	Glu	Phe	Val	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	Tyr	Lys	Asp
		115					120					125			
ctg	agg	aaa	ttt	ctg	gaa	agc	aaa	ggc	tac	gag	ttt	gag	tca	gaa	aca
Leu	Arg	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Glu	Phe	Glu	Ser	Glu	Thr
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Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Ile	Lys	Tyr	Val	Phe	Asp	Asn	Arg
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gaa	act	gag	gac	att	acg	ttt	tca	acg	ttg	gtc	gag	aga	gtc	att	cag
Glu	Thr	Glu	Asp	Ile	Thr	Phe	Ser	Thr	Leu	Val	Glu	Arg	Val	Ile	Gln
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Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	His	Tyr	Pro
			180					185					190		
gga	gaa	gcc	gtt	gcc	aca	cgg	aga	ggc	agc	ccc	ctg	ctc	atc	gga	gtc
Gly	Glu	Ala	Val	Ala	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	Ile	Gly	Val
		195					200					205			
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Arg	Ser	Lys	Tyr	Lys	Leu	Ser	Thr	Glu	Gln	Ile	Pro	Ile	Leu	Tyr	Arg
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Arg	Leu	Asp	Ser	Ser	Ala	Cys	Leu	His	Ala	Val	Gly	Asp	Lys	Ala	Val
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gaa	ttc	ttc	ttt	gct	tct	gat	gca	agc	gct	atc	ata	gag	cac	acc	aac
Glu	Phe	Phe	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Ile	Ile	Glu	His	Thr	Asn
			260					265					270		
cgg	gtc	atc	ttc	ctg	gag	gac	gat	gac	atc	gcc	gca	gtg	gct	gat	ggg
Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Ile	Ala	Ala	Val	Ala	Asp	Gly
		275					280					285			
aaa	ctc	tcc	att	cac	cgg	gtc	aag	cgc	tcg	gcc	agt	gat	gac	cca	tct
Lys	Leu	Ser	Ile	His	Arg	Val	Lys	Arg	Ser	Ala	Ser	Asp	Asp	Pro	Ser

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300

290	295																
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aac Asn	ttc Phe	agt Ser	gcg Ala	ttt Phe 325	atg Met	cag Gln	aag Lys	gag Glu	atc Ile 330	ttc Phe	gaa Glu	cag Gln	cca Pro	gaa Glu 335	tca Ser		1008
gtt Val	ttc Phe	aat Asn	act Thr 340	atg Met	aga Arg	ggt Gly	cgg Arg	gtg Val 345	aat Asn	ttt Phe	gaa Glu	acc Thr	aac Asn 350	aca Thr	gtg Val		1056
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cgg Arg 370	ctc Leu	atc Ile	gtg Val	att Ile	ggc Gly	tgt Cys 375	gga Gly	acc Thr	agc Ser	tac Tyr	cac His 380	gct Ala	gcc Ala	gtg Val	gct Ala		1152
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ctt Leu	gct Ala	agt Ser	gat Asp	ttt Phe 405	ctg Leu	gac Asp	agg Arg	aac Asn	aca Thr 410	cct Pro	gtg Val	ttc Phe	agg Arg	gat Asp 415	gac Asp		1248
gtt Val	tgc Cys	ttt Phe	ttc Phe 420	atc Ile	agc Ser	cag Gln	tca Ser	ggc Gly 425	gag Glu	acc Thr	gcg Ala	gac Asp	acc Thr 430	ctc Leu	ctg Leu		1296
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atc Ile 465	aac Asn	gca Ala	ggg Gly	ccg Pro	gag Glu 470	gtc Val	ggc Gly	gtg Val	gcc Ala	agc Ser 475	acc Thr	aag Lys	gct Ala	tat Tyr	acc Thr 480		1440
agt Ser	cag Gln	ttc Phe	atc Ile	tct Ser 485	ctg Leu	gtg Val	atg Met	ttt Phe	ggt Gly 490	ttg Leu	atg Met	atg Met	tct Ser	gaa Glu 495	gac Asp		1488
cga Arg	att Ile	tca Ser	cta Leu 500	caa Gln	aac Asn	agg Arg	agg Arg	caa Gln 505	gag Glu	atc Ile	atc Ile	cgt Arg	ggc Gly 510	ttg Leu	aga Arg		1536
tct Ser	tta Leu	cct Pro 515	gag Glu	ctg Leu	atc Ile	aag Lys	gaa Glu 520	gtg Val	ctg Leu	tct Ser	ctg Leu	gag Glu 525	gag Glu	aag Lys	atc Ile		1584
cac His	gac Asp 530	ttg Leu	gcc Ala	ctg Leu	gag Glu	ctc Leu 535	tac Tyr	acg Thr	cag Gln	aga Arg	tgc Ser 540	ctg Leu	ctg Leu	gtg Val	atg Met		1632

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ggg Gly 545	cgg Arg	ggc Gly	tac Tyr	aac Asn	tat Tyr 550	gcc Ala	acc Thr	tgc Cys	ctg Leu	gaa Glu 555	gga Gly	gcc Ala	ctg Leu	aaa Lys	att Ile 560	1680
aaa Lys	gag Glu	ata Ile	acc Thr	tac Tyr 565	atg Met	cac His	tca Ser	gaa Glu	ggc Gly 570	atc Ile	ctg Leu	gct Ala	ggg Gly	gag Glu 575	ctg Leu	1728
aag Lys	cac His	ggg Gly	ccc Pro 580	ctg Leu	gca Ala	ctg Leu	att Ile	gac Asp 585	aag Lys	cag Gln	atg Met	ccc Pro	gtc Val 590	atc Ile	atg Met	1776
gtc Val	att Ile	atg Met 595	aag Lys	gat Asp	cct Pro	tgc Cys	ttc Phe 600	gcc Ala	aaa Lys	tgc Cys	cag Gln	aac Asn 605	gcc Ala	ctg Leu	cag Gln	1824
caa Gln 610	gtc Val	acg Thr	gcc Ala	cgc Arg	cag Gln	ggg Gly 615	cgc Arg	ccc Pro	att Ile	ata Ile	ctg Leu 620	tgc Cys	tcc Ser	aag Lys	gac Asp	1872
gat Asp 625	act Thr	gaa Glu	agt Ser	tcc Ser	aag Lys 630	ttt Phe	gcg Ala	tat Tyr	aag Lys	aca Thr 635	atc Ile	gag Glu	ctg Leu	ccc Pro	cac His 640	1920
act Thr	gtg Val	gac Asp	tgc Cys	ctc Leu 645	cag Gln	ggc Gly	atc Ile	ctg Leu	agc Ser 650	gtg Val	att Ile	ccg Pro	ctg Leu	cag Gln 655	ctg Leu	1968
ctg Leu	tcc Ser	ttc Phe	cac His 660	ctg Leu	gct Ala	gtt Val	ctc Leu	cga Arg 665	gga Gly	tat Tyr	gac Asp	gtt Val	gac Asp 670	ttc Phe	ccc Pro	2016
aga Arg	aat Asn	ctg Leu 675	gcc Ala	aag Lys	tct Ser	gta Val	act Thr 680	gtg Val	gaa Glu	tga						2049

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 <212> PRT
 <213> Homo sapiens

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 Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu
 35 40 45
 Val Lys Glu Arg His Ile Gln Leu Val Lys Lys Arg Gly Lys Val Lys
 50 55 60
 Ala Leu Asp Glu Glu Leu Tyr Lys Gln Asp Ser Met Asp Leu Lys Val
 65 70 75 80
 Glu Phe Glu Thr His Phe Gly Ile Ala His Thr Arg Trp Ala Thr His
 85 90 95

Gly Val Pro Ser Ala Val Asn Ser His ^{GFAT-anglais} Pro Gln Arg Ser Asp Lys Gly
 100 105 110
 Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp
 115 120 125
 Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Glu Ser Glu Thr
 130 135 140
 Asp Thr Glu Thr Ile Ala Lys Leu Ile Lys Tyr Val Phe Asp Asn Arg
 145 150 155 160
 Glu Thr Glu Asp Ile Thr Phe Ser Thr Leu Val Glu Arg Val Ile Gln
 165 170 175
 Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val His Tyr Pro
 180 185 190
 Gly Glu Ala Val Ala Thr Arg Arg Gly Ser Pro Leu Leu Ile Gly Val
 195 200 205
 Arg Ser Lys Tyr Lys Leu Ser Thr Glu Gln Ile Pro Ile Leu Tyr Arg
 210 215 220
 Thr Cys Thr Leu Glu Asn Val Lys Asn Ile Cys Lys Thr Arg Met Lys
 225 230 235 240
 Arg Leu Asp Ser Ser Ala Cys Leu His Ala Val Gly Asp Lys Ala Val
 245 250 255
 Glu Phe Phe Phe Ala Ser Asp Ala Ser Ala Ile Ile Glu His Thr Asn
 260 265 270
 Arg Val Ile Phe Leu Glu Asp Asp Asp Ile Ala Ala Val Ala Asp Gly
 275 280 285
 Lys Leu Ser Ile His Arg Val Lys Arg Ser Ala Ser Asp Asp Pro Ser
 290 295 300
 Arg Ala Ile Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys Gly
 305 310 315 320
 Asn Phe Ser Ala Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu Ser
 325 330 335
 Val Phe Asn Thr Met Arg Gly Arg Val Asn Phe Glu Thr Asn Thr Val
 340 345 350
 Leu Leu Gly Gly Leu Lys Asp His Leu Lys Glu Ile Arg Arg Cys Arg
 355 360 365
 Arg Leu Ile Val Ile Gly Cys Gly Thr Ser Tyr His Ala Ala Val Ala
 370 375 380
 Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val Glu
 385 390 395 400
 Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp Asp
 405 410 415
 Val Cys Phe Phe Ile Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu Leu
 420 425 430

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Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala Leu Thr Val Gly Val Thr
435 440 445
Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val His
450 455 460
Ile Asn Ala Gly Pro Glu Val Gly Val Ala Ser Thr Lys Ala Tyr Thr
465 470 475 480
Ser Gln Phe Ile Ser Leu Val Met Phe Gly Leu Met Met Ser Glu Asp
485 490 495
Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu Ile Ile Arg Gly Leu Arg
500 505 510
Ser Leu Pro Glu Leu Ile Lys Glu Val Leu Ser Leu Glu Glu Lys Ile
515 520 525
His Asp Leu Ala Leu Glu Leu Tyr Thr Gln Arg Ser Leu Leu Val Met
530 535 540
Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys Ile
545 550 555 560
Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu Leu
565 570 575
Lys His Gly Pro Leu Ala Leu Ile Asp Lys Gln Met Pro Val Ile Met
580 585 590
Val Ile Met Lys Asp Pro Cys Phe Ala Lys Cys Gln Asn Ala Leu Gln
595 600 605
Gln Val Thr Ala Arg Gln Gly Arg Pro Ile Ile Leu Cys Ser Lys Asp
610 615 620
Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys Thr Ile Glu Leu Pro His
625 630 635 640
Thr Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln Leu
645 650 655
Leu Ser Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe Pro
660 665 670
Arg Asn Leu Ala Lys Ser Val Thr Val Glu
675 680

<210> 5
<211> 2100
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2100)
<223>

GFAT-anglais

<220>
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 <222> (170)..(170)
 <223> t or c

<400> 5

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Met	Cys	Gly	Ile	Phe	Ala	Tyr	Leu	Asn	Tyr	His	Val	Pro	Arg	Thr	Arg	
1				5					10					15		
cga	gaa	atc	ctg	gag	acc	cta	atc	aaa	ggc	ctt	cag	aga	ctg	gag	tac	96
Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
			20					25					30			
aga	gga	tat	gat	tct	gct	ggt	gtg	gga	ttt	gat	gga	ggc	aat	gat	aaa	144
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys	
		35					40					45				
gat	tgg	gaa	gcc	aat	gcc	tgc	aaa	anc	cag	ctt	att	aag	aag	aaa	gga	192
Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly	
	50					55					60					
aaa	gtt	aag	gca	ctg	gat	gaa	gaa	gtt	cac	aag	caa	caa	gat	atg	gat	240
Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp	
65					70					75					80	
ttg	gat	ata	gaa	ttt	gat	gta	cac	ctt	gga	ata	gct	cat	acc	cgt	tg	288
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp	
				85					90					95		
gca	aca	cat	gga	gaa	ccc	agt	cct	gtc	aat	agc	cac	ccc	cag	cgc	tct	336
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	
			100					105					110			
gat	aaa	aat	aat	gaa	ttt	atc	gtt	att	cac	aat	gga	atc	atc	acc	aac	384
Asp	Lys	Asn	Asn	Glu	Phe	Ile	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	
		115					120					125				
tac	aaa	gac	ttg	aaa	aag	ttt	ttg	gaa	agc	aaa	ggc	tat	gac	ttc	gaa	432
Tyr	Lys	Asp	Leu	Lys	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Asp	Phe	Glu	
	130					135					140					
tct	gaa	aca	gac	aca	gag	aca	att	gcc	aag	ctc	gtt	aag	tat	atg	tat	480
Ser	Glu	Thr	Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Val	Lys	Tyr	Met	Tyr	
145					150					155					160	
gac	aat	cgg	gaa	agt	caa	gat	acc	agc	ttt	act	acc	ttg	gtg	gag	aga	528
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg	
				165					170					175		
gtt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt	576
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	
			180					185					190			
cat	ttt	ccc	ggg	caa	gca	gtt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg	624
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	
		195					200					205				
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata	672
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile	
	210					215					220					

GFAT-anglais

ctc Leu 225	tac Tyr	aga Arg	aca Thr	gct Ala 230	agg Arg 230	act Thr	cag Gln	att Ile	gga Gly 235	tca Ser 235	aaa Lys	ttc Phe	aca Thr	cgg Arg	tgg Trp 240	720
gga Gly	tca Ser	cag Gln	gga Gly	gaa Glu 245	aga Arg	ggc Gly	aaa Lys	gac Asp	aag Lys 250	aaa Lys	gga Gly	agc Ser	tgc Cys	aat Asn 255	ctc Leu	768
tct Ser	cgt Arg	gtg Val	gac Asp 260	agc Ser	aca Thr	acc Thr	tgc Cys	ctt Leu 265	ttc Phe	ccg Pro	gtg Val	gaa Glu 270	gaa Glu 270	aaa Lys	gca Ala	816
gtg Val	gag Glu	tat Tyr 275	tac Tyr	ttt Phe	gct Ala	tct Ser	gat Asp 280	gca Ala	agt Ser	gct Ala	gtc Val	ata Ile 285	gaa Glu	cac His	acc Thr	864
aat Asn	cgc Arg 290	gtc Val	atc Ile	ttt Phe	ctg Leu	gaa Glu 295	gat Asp	gat Asp	gat Asp	gtt Val	gca Ala 300	gca Ala	gta Val	gtg Val	gat Asp	912
gga Gly 305	cgt Arg	ctt Leu	tct Ser	atc Ile	cat His 310	cga Arg	att Ile	aaa Lys	cga Arg	act Thr 315	gca Ala	gga Gly	gat Asp	cac His	ccc Pro 320	960
gga Gly	cga Arg	gct Ala	gtg Val	caa Gln 325	aca Thr	ctc Leu	cag Gln	atg Met	gaa Glu 330	ctc Leu	cag Gln	cag Gln	atc Ile	atg Met 335	aag Lys	1008
ggc Gly	aac Asn	ttc Phe	agt Ser 340	tca Ser	ttt Phe	atg Met	cag Gln	aag Lys 345	gaa Glu	ata Ile	ttt Phe	gag Glu	cag Gln 350	cca Pro	gag Glu	1056
tct Ser	gtc Val	gtg Val 355	aac Asn	aca Thr	atg Met	aga Arg	gga Gly 360	aga Arg	gtc Val	aac Asn	ttt Phe	gat Asp 365	gac Asp	tat Tyr	act Thr	1104
gtg Val	aat Asn 370	ttg Leu	ggt Gly	ggt Gly	ttg Leu	aag Lys 375	gat Asp	cac His	ata Ile	aag Lys	gag Glu 380	atc Ile	cag Gln	aga Arg	tgc Cys	1152
cgg Arg 385	cgt Arg	ttg Leu	att Ile	ctt Leu	att Ile 390	gct Ala	tgt Cys	gga Gly	aca Thr	agt Ser 395	tac Tyr	cat His	gct Ala	ggt Gly	gta Val 400	1200
gca Ala	aca Thr	cgt Arg	caa Gln	gtt Val 405	ctt Leu	gag Glu	gag Glu	ctg Leu	act Thr 410	gag Glu	ttg Leu	cct Pro	gtg Val 415	atg Met 415	gtg Val	1248
gaa Glu	cta Leu	gca Ala	agt Ser 420	gac Asp	ttc Phe	ctg Leu	gac Asp	aga Arg 425	aac Asn	aca Thr	cca Pro	gtc Val	ttt Phe 430	cga Arg	gat Asp	1296
gat Asp	gtt Val	tgc Cys 435	ttt Phe	ttc Phe	ctt Leu	agt Ser	caa Gln 440	tca Ser	ggt Gly	gag Glu	aca Thr	gca Ala 445	gat Asp	act Thr	ttg Leu	1344
atg Met	ggt Gly 450	ctt Leu	cgt Arg	tac Tyr	tgt Cys	aag Lys 455	gag Glu	aga Arg	gga Gly	gct Ala	tta Leu 460	act Thr	gtg Val	ggg Gly	atc Ile	1392

GFAT-anglais																
aca Thr 465	aac Asn	aca Thr	gtt Val	ggc Gly 470	agt Ser	tcc Ser	ata Ile	tca Ser	cgg Arg 475	gag Glu	aca Thr	gat Asp	tgt Cys	gga Gly 480	gtt Val 480	1440
cat His	att Ile	aat Asn	gct Ala	ggt Gly 485	cct Pro	gag Glu	att Ile	ggt Gly	gtg Val 490	gcc Ala	agt Ser	aca Thr	aag Lys	gct Ala 495	tat Tyr	1488
acc Thr	agc Ser	cag Gln	ttt Phe 500	gta Val	tcc Ser	ctt Leu	gtg Val	atg Met 505	ttt Phe	gcc Ala	ctt Leu	atg Met 510	atg Met 510	tgt Cys	gat Asp	1536
gat Asp	cgg Arg	atc Ile 515	tcc Ser	atg Met	caa Gln	gaa Glu	aga Arg 520	cgc Arg	aaa Lys	gag Glu	atc Ile	atg Met 525	ctt Leu	gga Gly	ttg Leu	1584
aaa Lys	cgg Arg 530	ctg Leu	cct Pro	gat Asp	ttg Leu	att Ile 535	aag Lys	gaa Glu	gta Val	ctg Leu	agc Ser 540	atg Met	gat Asp	gac Asp	gaa Glu	1632
att Ile 545	cag Gln	aaa Lys	cta Leu	gca Ala	aca Thr 550	gaa Glu	ctt Leu	tat Tyr	cat His	cag Gln 555	aag Lys	tca Ser	gtt Val	ctg Leu	ata Ile 560	1680
atg Met	gga Gly	cga Arg	ggc Gly	tat Tyr 565	cat His	tat Tyr	gct Ala	act Thr	tgt Cys 570	ctt Leu	gaa Glu	ggg Gly	gca Ala	ctg Leu 575	aaa Lys	1728
atc Ile	aaa Lys	gaa Glu	att Ile 580	act Thr	tat Tyr	atg Met	cac His	tct Ser 585	gaa Glu	ggc Gly	atc Ile	ctt Leu	gct Ala 590	ggt Gly	gaa Glu	1776
ttg Leu	aaa Lys	cat His 595	ggc Gly	cct Pro	ctg Leu	gct Ala	ttg Leu 600	gtg Val	gat Asp	aaa Lys	ttg Leu	atg Met 605	cct Pro	gtg Val	atc Ile	1824
atg Met	atc Ile 610	atc Ile	atg Met	aga Arg	gat Asp	cac His 615	act Thr	tat Tyr	gcc Ala	aag Lys	tgt Cys 620	cag Gln	aat Asn	gct Ala	ctt Leu	1872
cag Gln 625	caa Gln	gtg Val	gtt Val	gct Ala	cgg Arg 630	cag Gln	ggg Gly	cgg Arg	cct Pro	gtg Val 635	gta Val	att Ile	tgt Cys	gat Asp	aag Lys 640	1920
gag Glu	gat Asp	act Thr	gag Glu	acc Thr 645	att Ile	aag Lys	aac Asn	aca Thr	aaa Lys 650	aga Arg	acg Thr	atc Ile	aag Lys	gtg Val 655	ccc Pro	1968
cac His	tca Ser	gtg Val	gac Asp 660	tgc Cys	ttg Leu	cag Gln	ggc Gly	att Ile 665	ctc Leu	agc Ser	gtg Val	atc Ile	cct Pro 670	tta Leu	cag Gln	2016
ttg Leu	ctg Leu	gct Ala 675	ttc Phe	cac His	ctt Leu	gct Ala	gtg Val 680	ctg Leu	aga Arg	ggc Gly	tat Tyr	gat Asp 685	gtt Val	gat Asp	ttc Phe	2064
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GFAT-anglais

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 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (57)..(57)
 <223> 'Xaa' in position 57 represents Thr or Ile

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 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys
 35 40 45
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
 50 55 60
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
 65 70 75 80
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp
 85 90 95
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser
 100 105 110
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn
 115 120 125
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu
 130 135 140
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr
 145 150 155 160
 Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg
 165 170 175
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val
 180 185 190
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu
 195 200 205
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile
 210 215 220
 Leu Tyr Arg Thr Ala Arg Thr Gln Ile Gly Ser Lys Phe Thr Arg Trp
 225 230 235 240
 Gly Ser Gln Gly Glu Arg Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu
 245 250 255
 Ser Arg Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala
 260 265 270
 Val Glu Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr

GFAT-anglais

275	280	285
Asn Arg Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp		
290 295 300		
Gly Arg Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro		
305 310 315 320		
Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys		
325 330 335		
Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu		
340 345 350		
Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr		
355 360 365		
Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys		
370 375 380		
Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val		
385 390 395 400		
Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val		
405 410 415		
Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp		
420 425 430		
Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu		
435 440 445		
Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile		
450 455 460		
Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val		
465 470 475 480		
His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr		
485 490 495		
Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp		
500 505 510		
Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu		
515 520 525		
Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu		
530 535 540		
Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile		
545 550 555 560		
Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys		
565 570 575		
Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu		
580 585 590		
Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile		
595 600 605		

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Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu
610 615 620
Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys
625 630 635 640
Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro
645 650 655
His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln
660 665 670
Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe
675 680 685
Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
690 695

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<212> DNA
<213> Artificial sequence

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<222> (1)..(2064)
<223>

<220>
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cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac 96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr
20 25 30
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa 144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys
35 40 45
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga 192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
50 55 60
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat 240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
65 70 75 80
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg 288

									GFAT-anglais									
Leu	Asp	Ile	Glu	Phe 85	Asp	Val	His	Leu	Gly 90	Ile	Ala	His	Thr	Arg 95	Trp			
gca Ala	aca Thr	cat His	gga Gly 100	gaa Glu	ccc Pro	agt Ser	cct Pro	gtc Val 105	aat Asn	agc Ser	cac His	ccc Pro	cag Gln 110	cgc Arg	tct Ser	336		
gat Asp	aaa Lys	aat Asn 115	aat Asn	gaa Glu	ttt Phe	atc Ile	gtt Val 120	att Ile	cac His	aat Asn	gga Gly	atc Ile 125	atc Ile	acc Thr	aac Asn	384		
tac Tyr	aaa Lys 130	gac Asp	ttg Leu	aaa Lys	aag Lys	ttt Phe 135	ttg Leu	gaa Glu	agc Ser	aaa Lys	ggc Gly 140	tat Tyr	gac Asp	ttc Phe	gaa Glu	432		
tct Ser 145	gaa Glu	aca Thr	gac Asp	aca Thr	gag Glu 150	aca Thr	att Ile	gcc Ala	aag Lys	ctc Leu 155	gtt Val	aag Lys	tat Tyr	atg Met	tat Tyr 160	480		
gac Asp	aat Asn	cgg Arg	gaa Glu	agt Ser 165	caa Gln	gat Asp	acc Thr	agc Ser	ttt Phe 170	act Thr	acc Thr	ttg Leu	gtg Val	gag Glu 175	aga Arg	528		
gtt Val	atc Ile	caa Gln 180	caa Gln	ttg Leu	gaa Glu	ggc Gly	gct Ala	ttt Phe 185	gca Ala	ctt Leu	gtg Val	ttt Phe 190	aaa Lys	agt Ser	gtt Val	576		
cat His	ttt Phe	ccc Pro 195	ggg Gly	caa Gln	gca Ala	gtt Val	ggc Gly 200	aca Thr	agg Arg	cga Arg	ggc Gly	agc Ser 205	cct Pro	ctg Leu	ttg Leu	624		
att Ile	ggc Gly 210	gta Val	cgg Arg	agt Ser	gaa Glu	cat His 215	aaa Lys	ctt Leu	tct Ser	act Thr	gat Asp 220	cac His	att Ile	cct Pro	ata Ile	672		
ctc Leu 225	tac Tyr	aga Arg	aca Thr	ggc Gly	aaa Lys 230	gac Asp	aag Lys	aaa Lys	gga Gly	agc Ser 235	tgc Cys	aat Asn	ctc Leu	tct Ser	cgt Arg 240	720		
gtg Val	gac Asp	agc Ser	aca Thr	acc Thr 245	tgc Cys	ctt Leu	ttc Phe	ccg Pro	gtg Val 250	gaa Glu	gaa Glu	aaa Lys	gca Ala	gtg Val 255	gag Glu	768		
tat Tyr	tac Tyr	ttt Phe	gct Ala 260	tct Ser	gat Asp	gca Ala	agt Ser	gct Ala 265	gtc Val	ata Ile	gaa Glu	cac His	acc Thr 270	aat Asn	cgc Arg	816		
gtc Val	atc Ile	ttt Phe 275	ctg Leu	gaa Glu	gat Asp	gat Asp	gat Asp 280	gtt Val	gca Ala	gca Ala	gta Val	gtg Val 285	gat Asp	gga Gly	cgt Arg	864		
ctt Leu	tct Ser 290	atc Ile	cat His	cga Arg	att Ile	aaa Lys 295	cga Arg	act Thr	gca Ala	gga Gly	cat His 300	cac His	cat His	cac His	cat His	912		
cac His 305	gat Asp	cac His	ccc Pro	gga Gly	cga Arg 310	gct Ala	gtg Val	caa Gln	aca Thr	ctc Leu 315	cag Gln	atg Met	gaa Glu	ctc Leu	cag Gln 320	960		
cag Gln	atc Ile	atg Met	aag Lys	ggc Gly 325	aac Asn	ttc Phe	agt Ser	tca Ser	ttt Phe 330	atg Met	cag Gln	aag Lys	gaa Glu	ata Ile 335	ttt Phe	1008		

GFAT-anglais																
gag Glu	cag Gln	cca Pro	gag Glu 340	tct Ser	gtc Val	gtg Val	aac Asn	aca Thr 345	atg Met	aga Arg	gga Gly	aga Arg	gtc Val 350	aac Asn	ttt Phe	1056
gat Asp	gac Asp	tat Tyr 355	act Thr	gtg Val	aat Asn	ttg Leu	ggt Gly 360	ggt Gly	ttg Leu	aag Lys	gat Asp	cac His 365	ata Ile	aag Lys	gag Glu	1104
atc Ile	cag Gln 370	aga Arg	tgc Cys	cgg Arg	cgt Arg	ttg Leu 375	att Ile	ctt Leu	att Ile	gct Ala	tgt Cys 380	gga Gly	aca Thr	agt Ser	tac Tyr	1152
cat His 385	gct Ala	ggt Gly	gta Val	gca Ala	aca Thr 390	cgt Arg	caa Gln	ggt Val	ctt Leu	gag Glu 395	gag Glu	ctg Leu	act Thr	gag Glu	ttg Leu 400	1200
cct Pro	gtg Val	atg Met	gtg Val	gaa Glu 405	cta Leu	gca Ala	agt Ser	gac Asp	ttc Phe 410	ctg Leu	gac Asp	aga Arg	aac Asn	aca Thr 415	cca Pro	1248
gtc Val	ttt Phe	cga Arg	gat Asp 420	gat Asp	gtt Val	tgc Cys	ttt Phe	ttc Phe 425	ctt Leu	agt Ser	caa Gln	tca Ser	ggt Gly 430	gag Glu	aca Thr	1296
gca Ala	gat Asp	act Thr 435	ttg Leu	atg Met	ggt Gly	ctt Leu	cgt Arg 440	tac Tyr	tgt Cys	aag Lys	gag Glu	aga Arg 445	gga Gly	gct Ala	tta Leu	1344
act Thr	gtg Val 450	ggg Gly	atc Ile	aca Thr	aac Asn	aca Thr 455	ggt Val	ggc Gly	agt Ser	tcc Ser	ata Ile 460	tca Ser	cgg Arg	gag Glu	aca Thr	1392
gat Asp 465	tgt Cys	gga Gly	gtt Val	cat His	att Ile 470	aat Asn	gct Ala	ggt Gly	cct Pro	gag Glu 475	att Ile	ggt Gly	gtg Val	gcc Ala	agt Ser 480	1440
aca Thr	aag Lys	gct Ala	tat Tyr	acc Thr 485	agc Ser	cag Gln	ttt Phe	gta Val	tcc Ser 490	ctt Leu	gtg Val	atg Met	ttt Phe	gcc Ala 495	ctt Leu	1488
atg Met	atg Met	tgt Cys	gat Asp 500	gat Asp	cgg Arg	atc Ile	tcc Ser	atg Met 505	caa Gln	gaa Glu	aga Arg	cgc Arg	aaa Lys 510	gag Glu	atc Ile	1536
atg Met	ctt Leu	gga Gly 515	ttg Leu	aaa Lys	cgg Arg	ctg Leu	cct Pro 520	gat Asp	ttg Leu	att Ile	aag Lys	gaa Glu 525	gta Val	ctg Leu	agc Ser	1584
atg Met	gat Asp 530	gac Asp	gaa Glu	att Ile	cag Gln	aaa Lys 535	cta Leu	gca Ala	aca Thr	gaa Glu	ctt Leu 540	tat Tyr	cat His	cag Gln	aag Lys	1632
tca Ser 545	gtt Val	ctg Leu	ata Ile	atg Met	gga Gly 550	cga Arg	ggc Gly	tat Tyr	cat His	tat Tyr 555	gct Ala	act Thr	tgt Cys	ctt Leu	gaa Glu 560	1680
ggg Gly	gca Ala	ctg Leu	aaa Lys	atc Ile 565	aaa Lys	gaa Glu	att Ile	act Thr	tat Tyr 570	atg Met	cac His	tct Ser	gaa Glu	ggc Gly 575	atc Ile	1728
ctt	gct	ggt	gaa	ttg	aaa	cat	ggc	cct	ctg	gct	ttg	gtg	gat	aaa	ttg	1776

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Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu	
			580					585					590			
atg	cct	gtg	atc	atg	atc	atc	atg	aga	gat	cac	act	tat	gcc	aag	tgt	1824
Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys	
		595					600					605				
cag	aat	gct	ctt	cag	caa	gtg	ggt	gct	cgg	cag	ggg	cgg	cct	gtg	gta	1872
Gln	Asn	Ala	Leu	Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	Val	Val	
	610					615					620					
att	tgt	gat	aag	gag	gat	act	gag	acc	att	aag	aac	aca	aaa	aga	acg	1920
Ile	Cys	Asp	Lys	Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	Arg	Thr	
	625				630					635					640	
atc	aag	gtg	ccc	cac	tca	gtg	gac	tgc	ttg	cag	ggc	att	ctc	agc	gtg	1968
Ile	Lys	Val	Pro	His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	
				645					650					655		
atc	cct	tta	cag	ttg	ctg	gct	ttc	cac	ctt	gct	gtg	ctg	aga	ggc	tat	2016
Ile	Pro	Leu	Gln	Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	
			660					665					670			
gat	gtt	gat	ttc	cca	cgg	aat	ctt	gcc	aaa	tct	gtg	act	gta	gag	tga	2064
Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu		
		675					680					685				

<210> 8
 <211> 687
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (57)..(57)
 <223> 'Xaa' in position 57 represents Thr or Ile

<220>
 <223> modified GFAT1 by an internal purification tag

<400> 8
 Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg
 1 5 10 15
 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr
 20 25 30
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys
 35 40 45
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly
 50 55 60
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp
 65 70 75 80
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp
 85 90 95
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser
 100 105 110

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Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn
115 120 125

Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu
130 135 140

Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr
145 150 155 160

Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg
165 170 175

Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val
180 185 190

His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu
195 200 205

Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile
210 215 220

Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg
225 230 235 240

Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu
245 250 255

Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg
260 265 270

Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg
275 280 285

Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly His His His His His
290 295 300

His Asp His Pro Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln
305 310 315 320

Gln Ile Met Lys Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe
325 330 335

Glu Gln Pro Glu Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe
340 345 350

Asp Asp Tyr Thr Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu
355 360 365

Ile Gln Arg Cys Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr
370 375 380

His Ala Gly Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu
385 390 395 400

Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro
405 410 415

Val Phe Arg Asp Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr
420 425 430

Ala Asp Thr Leu Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu

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435 440 445

Thr Val Gly Ile Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr
450 455 460

Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser
465 470 475 480

Thr Lys Ala Tyr Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu
485 490 495

Met Met Cys Asp Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile
500 505 510

Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser
515 520 525

Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys
530 535 540

Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu
545 550 555 560

Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile
565 570 575

Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu
580 585 590

Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys
595 600 605

Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val
610 615 620

Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr
625 630 635 640

Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val
645 650 655

Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr
660 665 670

Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
675 680 685

<210> 9
<211> 2067
<212> DNA
<213> Artificial sequence

<220>
<223> modified GFAT2 by an internal purification tag

<220>
<221> CDS
<222> (1)..(2067)
<223>

<400> 9

GFAT-anglais																
atg Met 1	tgc Cys	gga Gly	atc Ile	ttt Phe 5	gcc Ala	tac Tyr	atg Met	aac Asn	tac Tyr 10	aga Arg	gtc Val	ccc Pro	cgg Arg	acg Thr 15	agg Arg	48
aag Lys	gag Glu	atc Ile	ttc Phe 20	gaa Glu	acc Thr	ctc Leu	atc Ile	aag Lys 25	ggc Gly	ctg Leu	cag Gln	cgg Arg	ctg Leu 30	gag Glu	tac Tyr	96
aga Arg	ggc Gly	tac Tyr 35	gac Asp	tcg Ser	gca Ala	ggt Gly	gtg Val 40	gcg Ala	atc Ile	gat Asp	ggg Gly	aat Asn 45	aat Asn	cac His	gaa Glu	144
gtc Val	aaa Lys 50	gaa Glu	aga Arg	cac His	att Ile	cag Gln 55	ctg Leu	gtc Val	aag Lys	aaa Lys	agg Arg 60	ggg Gly	aaa Lys	gtc Val	aag Lys	192
gct Ala 65	ctc Leu	gat Asp	gaa Glu	gaa Glu	ctt Leu 70	tac Tyr	aaa Lys	caa Gln	gac Asp	agc Ser 75	atg Met	gac Asp	tta Leu	aaa Lys	gtg Val 80	240
gag Glu	ttt Phe	gag Glu	aca Thr	cac His 85	ttc Phe	ggc Gly	att Ile	gcc Ala	cac His 90	acg Thr	cgc Arg	tgg Trp	gcc Ala	acc Thr 95	cac His	288
ggg Gly	gtc Val	ccc Pro	agt Ser 100	gct Ala	gtc Val	aac Asn	agc Ser	cac His 105	cct Pro	cag Gln	cgc Arg	tca Ser	gac Asp 110	aaa Lys	ggc Gly	336
aac Asn	gaa Glu	ttt Phe 115	gtt Val	gtc Val	atc Ile	cac His	aat Asn 120	ggg Gly	atc Ile	atc Ile	aca Thr	aat Asn 125	tac Tyr	aaa Lys	gat Asp	384
ctg Leu	agg Arg 130	aaa Lys	ttt Phe	ctg Leu	gaa Glu	agc Ser 135	aaa Lys	ggc Gly	tac Tyr	gag Glu	ttt Phe 140	gag Glu	tca Ser	gaa Glu	aca Thr	432
gat Asp 145	aca Thr	gag Glu	acc Thr	atc Ile	gcc Ala 150	aag Lys	ctg Leu	att Ile	aaa Lys	tat Tyr 155	gtg Val	ttc Phe	gac Asp	aac Asn	aga Arg 160	480
gaa Glu	act Thr	gag Glu	gac Asp	att Ile 165	acg Thr	ttt Phe	tca Ser	acg Thr	ttg Leu 170	gtc Val	gag Glu	aga Arg	gtc Val	att Ile 175	cag Gln	528
cag Gln	ttg Leu	gaa Glu	ggt Gly 180	gca Ala	ttc Phe	gcg Ala	ctg Leu	gtt Val 185	ttc Phe	aag Lys	agt Ser	gtc Val	cac His 190	tac Tyr	cca Pro	576
gga Gly	gaa Glu	gcc Ala 195	gtt Val	gcc Ala	aca Thr	cgg Arg	aga Arg 200	ggc Gly	agc Ser	ccc Pro	ctg Leu	ctc Leu 205	atc Ile	gga Gly	gtc Val	624
cgg Arg	agc Ser 210	aaa Lys	tac Tyr	aag Lys	ctc Leu	tcc Ser 215	aca Thr	gaa Glu	cag Gln	atc Ile	cct Pro 220	atc Ile	tta Leu	tac Tyr	agg Arg	672
acg Thr 225	tgc Cys	act Thr	ctg Leu	gag Glu	aat Asn 230	gtg Val	aag Lys	aat Asn	atc Ile	tgt Cys 235	aag Lys	aca Thr	cgg Arg	atg Met	aag Lys 240	720
agg Arg	ctg Leu	gac Asp	agc Ser	tcc Ser 245	gcc Ala	tgc Cys	ctg Leu	cat His	gct Ala 250	gtg Val	ggc Gly	gac Asp	aag Lys	gcc Ala 255	gtg Val	768

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gaa Glu	ttc Phe	ttc Phe	ttt Phe 260	gct Ala	tct Ser	gat Asp	gca Ala	agc Ser 265	gct Ala	atc Ile	ata Ile	gag Glu	cac His 270	acc Thr	aac Asn	816
cgg Arg	gtc Val	atc Ile 275	ttc Phe	ctg Leu	gag Glu	gac Asp	gat Asp 280	gac Asp	atc Ile	gcc Ala	gca Ala	gtg Val 285	gct Ala	gat Asp	ggg Gly	864
aaa Lys	ctc Leu 290	tcc Ser	att Ile	cac His	cgg Arg	gtc Val 295	aag Lys	cgc Arg	tcg Ser	gcc Ala	agt Ser 300	cat His	cac His	cat His	cac His	912
cat His 305	cac His	gat Asp	gac Asp	cca Pro	tct Ser 310	cga Arg	gcc Ala	atc Ile	cag Gln	acc Thr 315	ttg Leu	cag Gln	atg Met	gaa Glu	ctg Leu 320	960
cag Gln	caa Gln	atc Ile	atg Met	aaa Lys 325	ggt Gly	aac Asn	ttc Phe	agt Ser	gcg Ala 330	ttt Phe	atg Met	cag Gln	aag Lys	gag Glu 335	atc Ile	1008
ttc Phe	gaa Glu	cag Gln	cca Pro 340	gaa Glu	tca Ser	gtt Val	ttc Phe	aat Asn 345	act Thr	atg Met	aga Arg	ggt Gly	cgg Arg 350	gtg Val	aat Asn	1056
ttt Phe	gaa Glu	acc Thr 355	aac Asn	aca Thr	gtg Val	ctc Leu	ctg Leu 360	ggt Gly	ggc Gly	ttg Leu	aag Lys	gac Asp 365	cac His	ttg Leu	aag Lys	1104
gag Glu	att Ile 370	cga Arg	cga Arg	tgc Cys	cga Arg	cgg Arg 375	ctc Leu	atc Ile	gtg Val	att Ile	ggc Gly 380	tgt Cys	gga Gly	acc Thr	agc Ser	1152
tac Tyr 385	cac His	gct Ala	gcc Ala	gtg Val	gct Ala 390	acg Thr	cgg Arg	caa Gln	gtt Val	ttg Leu 395	gag Glu	gaa Glu	ctg Leu	act Thr	gag Glu 400	1200
ctt Leu	cct Pro	gtg Val	atg Met	gtt Val 405	gaa Glu	ctt Leu	gct Ala	agt Ser	gat Asp 410	ttt Phe	ctg Leu	gac Asp	agg Arg	aac Asn 415	aca Thr	1248
cct Pro	gtg Val	ttc Phe	agg Arg 420	gat Asp	gac Asp	gtt Val	tgc Cys	ttt Phe 425	ttc Phe	atc Ile	agc Ser	cag Gln	tca Ser 430	ggc Gly	gag Glu	1296
acc Thr	gcg Ala	gac Asp 435	acc Thr	ctc Leu	ctg Leu	gcg Ala	ctg Leu 440	cgc Arg	tac Tyr	tgt Cys	aag Lys	gac Asp 445	cgc Arg	ggc Gly	gct Ala	1344
ctc Leu	acc Thr 450	gtg Val	ggc Gly	gtc Val	acc Thr	aac Asn 455	acc Thr	gtg Val	ggc Gly	agc Ser	tcc Ser 460	atc Ile	tct Ser	cgc Arg	gag Glu	1392
acc Thr 465	gac Asp	tgc Cys	ggc Gly	gtc Val	cac His 470	atc Ile	aac Asn	gca Ala	ggg Gly	ccg Pro 475	gag Glu	gtc Val	ggc Gly	gtg Val	gcc Ala 480	1440
agc Ser	acc Thr	aag Lys	gct Ala 485	tat Tyr	acc Thr	agt Ser	cag Gln	ttc Phe	atc Ile 490	tct Ser	ctg Leu	gtg Val	atg Met	ttt Phe 495	ggt Gly	1488
ttg Leu	atg Met	atg Met	tct Ser	gaa Glu	gac Asp	cga Arg	att Ile	tca Ser	cta Leu	caa Gln	aac Asn	agg Arg	agg Arg	caa Gln	gag Glu	1536

GFAT-anglais																
500					505					510						
atc Ile	atc Ile	cgt Arg 515	ggc Gly	ttg Leu	aga Arg	tct Ser	tta Leu 520	cct Pro	gag Glu	ctg Leu	atc Ile	aag Lys 525	gaa Glu	gtg Val	ctg Leu	1584
tct Ser	ctg Leu 530	gag Glu	gag Glu	aag Lys	atc Ile	cac His 535	gac Asp	ttg Leu	gcc Ala	ctg Leu	gag Glu 540	ctc Leu	tac Tyr	acg Thr	cag Gln	1632
aga Arg 545	tcg Ser	ctg Leu	ctg Leu	gtg Val	atg Met 550	ggg Gly	cgg Arg	ggc Gly	tac Tyr	aac Asn 555	tat Tyr	gcc Ala	acc Thr	tgc Cys	ctg Leu 560	1680
gaa Glu	gga Gly	gcc Ala	ctg Leu	aaa Lys 565	att Ile	aaa Lys	gag Glu	ata Ile	acc Thr 570	tac Tyr	atg Met	cac His	tca Ser	gaa Glu 575	ggc Gly	1728
atc Ile	ctg Leu	gct Ala	ggg Gly 580	gag Glu	ctg Leu	aag Lys	cac His	ggg Gly 585	ccc Pro	ctg Leu	gca Ala	ctg Leu	att Ile 590	gac Asp	aag Lys	1776
cag Gln	atg Met	ccc Pro 595	gtc Val	atc Ile	atg Met	gtc Val	att Ile 600	atg Met	aag Lys	gat Asp	cct Pro	tgc Cys 605	ttc Phe	gcc Ala	aaa Lys	1824
tgc Cys	cag Gln 610	aac Asn	gcc Ala	ctg Leu	cag Gln	caa Gln 615	gtc Val	acg Thr	gcc Ala	cgc Arg	cag Gln 620	ggg Gly	cgc Arg	ccc Pro	att Ile	1872
ata Ile 625	ctg Leu	tgc Cys	tcc Ser	aag Lys	gac Asp 630	gat Asp	act Thr	gaa Glu	agt Ser	tcc Ser 635	aag Lys	ttt Phe	gcg Ala	tat Tyr	aag Lys 640	1920
aca Thr	atc Ile	gag Glu	ctg Leu	ccc Pro 645	cac His	act Thr	gtg Val	gac Asp	tgc Cys 650	ctc Leu	cag Gln	ggc Gly	atc Ile	ctg Leu 655	agc Ser	1968
gtg Val	att Ile	ccg Pro	ctg Leu 660	cag Gln	ctg Leu	ctg Leu	tcc Ser	ttc Phe 665	cac His	ctg Leu	gct Ala	gtt Val	ctc Leu 670	cga Arg	gga Gly	2016
tat Tyr	gac Asp	gtt Val 675	gac Asp	ttc Phe	ccc Pro	aga Arg	aat Asn 680	ctg Leu	gcc Ala	aag Lys	tct Ser	gta Val 685	act Thr	gtg Val	gaa Glu	2064
tga																2067

<210> 10
 <211> 688
 <212> PRT
 <213> Artificial sequence

<220>
 <223> modified GFAT2 by an internal purification tag

<400> 10
 Met Cys Gly Ile Phe Ala Tyr Met Asn Tyr Arg Val Pro Arg Thr Arg
 1 5 10 15

Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr

GFAT-anglais

20					25					30					
Arg	Gly	Tyr ₃₅	Asp	Ser	Ala	Gly	Val ₄₀	Ala	Ile	Asp	Gly	Asn ₄₅	Asn	His	Glu
Val	Lys ₅₀	Glu	Arg	His	Ile	Gln ₅₅	Leu	Val	Lys	Lys	Arg ₆₀	Gly	Lys	Val	Lys
Ala ₆₅	Leu	Asp	Glu	Glu	Leu ₇₀	Tyr	Lys	Gln	Asp	Ser ₇₅	Met	Asp	Leu	Lys	Val ₈₀
Glu	Phe	Glu	Thr	His ₈₅	Phe	Gly	Ile	Ala	His ₉₀	Thr	Arg	Trp	Ala	Thr ₉₅	His
Gly	Val	Pro	Ser ₁₀₀	Ala	Val	Asn	Ser	His ₁₀₅	Pro	Gln	Arg	Ser	Asp ₁₁₀	Lys	Gly
Asn	Glu	Phe ₁₁₅	Val	Val	Ile	His	Asn ₁₂₀	Gly	Ile	Ile	Thr	Asn ₁₂₅	Tyr	Lys	Asp
Leu	Arg ₁₃₀	Lys	Phe	Leu	Glu	Ser ₁₃₅	Lys	Gly	Tyr	Glu	Phe ₁₄₀	Glu	Ser	Glu	Thr
Asp ₁₄₅	Thr	Glu	Thr	Ile	Ala ₁₅₀	Lys	Leu	Ile	Lys	Tyr ₁₅₅	Val	Phe	Asp	Asn	Arg ₁₆₀
Glu	Thr	Glu	Asp	Ile ₁₆₅	Thr	Phe	Ser	Thr	Leu ₁₇₀	Val	Glu	Arg	Val	Ile ₁₇₅	Gln
Gln	Leu	Glu	Gly ₁₈₀	Ala	Phe	Ala	Leu	Val ₁₈₅	Phe	Lys	Ser	Val	His ₁₉₀	Tyr	Pro
Gly	Glu	Ala ₁₉₅	Val	Ala	Thr	Arg	Arg ₂₀₀	Gly	Ser	Pro	Leu	Leu ₂₀₅	Ile	Gly	Val
Arg	Ser ₂₁₀	Lys	Tyr	Lys	Leu	Ser ₂₁₅	Thr	Glu	Gln	Ile	Pro ₂₂₀	Ile	Leu	Tyr	Arg
Thr ₂₂₅	Cys	Thr	Leu	Glu	Asn ₂₃₀	Val	Lys	Asn	Ile	Cys ₂₃₅	Lys	Thr	Arg	Met	Lys ₂₄₀
Arg	Leu	Asp	Ser	Ser ₂₄₅	Ala	Cys	Leu	His	Ala ₂₅₀	Val	Gly	Asp	Lys	Ala ₂₅₅	Val
Glu	Phe	Phe	Phe ₂₆₀	Ala	Ser	Asp	Ala	Ser ₂₆₅	Ala	Ile	Ile	Glu	His ₂₇₀	Thr	Asn
Arg	Val	Ile ₂₇₅	Phe	Leu	Glu	Asp	Asp ₂₈₀	Asp	Ile	Ala	Ala	Val ₂₈₅	Ala	Asp	Gly
Lys	Leu ₂₉₀	Ser	Ile	His	Arg	Val ₂₉₅	Lys	Arg	Ser	Ala	Ser ₃₀₀	His	His	His	His
His ₃₀₅	His	Asp	Asp	Pro	Ser ₃₁₀	Arg	Ala	Ile	Gln	Thr ₃₁₅	Leu	Gln	Met	Glu	Leu ₃₂₀
Gln	Gln	Ile	Met	Lys ₃₂₅	Gly	Asn	Phe	Ser	Ala ₃₃₀	Phe	Met	Gln	Lys	Glu ₃₃₅	Ile
Phe	Glu	Gln	Pro ₃₄₀	Glu	Ser	Val	Phe	Asn ₃₄₅	Thr	Met	Arg	Gly	Arg ₃₅₀	Val	Asn
Phe	Glu	Thr	Asn	Thr	Val	Leu	Leu	Gly	Gly	Leu	Lys	Asp	His	Leu	Lys

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355		360		365
Glu Ile Arg Arg Cys Arg Arg	Leu Ile Val Ile Gly Cys Gly Thr Ser			
370	375	380		
Tyr His Ala Ala Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu				
385	390	395		400
Leu Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr				
	405	410		415
Pro Val Phe Arg Asp Asp Val Cys Phe Phe Ile Ser Gln Ser Gly Glu				
	420	425		430
Thr Ala Asp Thr Leu Leu Ala Leu Arg Tyr Cys Lys Asp Arg Gly Ala				
	435	440		445
Leu Thr Val Gly Val Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu				
	450	455		460
Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Val Gly Val Ala				
	465	470		475
Ser Thr Lys Ala Tyr Thr Ser Gln Phe Ile Ser Leu Val Met Phe Gly				
	485	490		495
Leu Met Met Ser Glu Asp Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu				
	500	505		510
Ile Ile Arg Gly Leu Arg Ser Leu Pro Glu Leu Ile Lys Glu Val Leu				
	515	520		525
Ser Leu Glu Glu Lys Ile His Asp Leu Ala Leu Glu Leu Tyr Thr Gln				
	530	535		540
Arg Ser Leu Leu Val Met Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu				
	545	550		555
Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly				
	565	570		575
Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Lys				
	580	585		590
Gln Met Pro Val Ile Met Val Ile Met Lys Asp Pro Cys Phe Ala Lys				
	595	600		605
Cys Gln Asn Ala Leu Gln Gln Val Thr Ala Arg Gln Gly Arg Pro Ile				
	610	615		620
Ile Leu Cys Ser Lys Asp Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys				
	625	630		635
Thr Ile Glu Leu Pro His Thr Val Asp Cys Leu Gln Gly Ile Leu Ser				
	645	650		655
Val Ile Pro Leu Gln Leu Leu Ser Phe His Leu Ala Val Leu Arg Gly				
	660	665		670
Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu				
	675	680		685

GFAT-anglais

<210> 11
 <211> 2118
 <212> DNA
 <213> Artificial sequence

<220>
 <223> modified GFAT1Alt by an internal purification tag

<220>
 <221> CDS
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 <223>

<220>
 <221> misc_feature
 <222> (170)..(170)
 <223> t or c

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Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg		
1 5 10 15		
cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac		96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr		
20 25 30		
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa		144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Asn Asp Lys		
35 40 45		
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga		192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly		
50 55 60		
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat		240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp		
65 70 75 80		
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg		288
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp		
85 90 95		
gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct		336
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser		
100 105 110		
gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac		384
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn		
115 120 125		
tac aaa gac ttg aaa aag ttt ttg gaa agc aaa ggc tat gac ttc gaa		432
Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu		
130 135 140		
tct gaa aca gac aca gag aca att gcc aag ctc gtt aag tat atg tat		480
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr		
145 150 155 160		
gac aat cgg gaa agt caa gat acc agc ttt act acc ttg gtg gag aga		528

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Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg	
				165					170					175		
gtt	atc	caa	caa	ttg	gaa	ggt	gct	ttt	gca	ctt	gtg	ttt	aaa	agt	gtt	576
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	
			180					185					190			
cat	ttt	ccc	ggg	caa	gca	gtt	ggc	aca	agg	cga	ggt	agc	cct	ctg	ttg	624
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	
		195					200					205				
att	ggt	gta	cgg	agt	gaa	cat	aaa	ctt	tct	act	gat	cac	att	cct	ata	672
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile	
	210					215					220					
ctc	tac	aga	aca	gct	agg	act	cag	att	gga	tca	aaa	ttc	aca	cgg	tgg	720
Leu	Tyr	Arg	Thr	Ala	Arg	Thr	Gln	Ile	Gly	Ser	Lys	Phe	Thr	Arg	Trp	
					230					235					240	
gga	tca	cag	gga	gaa	aga	ggc	aaa	gac	aag	aaa	gga	agc	tgc	aat	ctc	768
Gly	Ser	Gln	Gly	Glu	Arg	Gly	Lys	Asp	Lys	Lys	Gly	Ser	Cys	Asn	Leu	
				245					250					255		
tct	cgt	gtg	gac	agc	aca	acc	tgc	ctt	ttc	ccg	gtg	gaa	gaa	aaa	gca	816
Ser	Arg	Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala	
			260					265					270			
gtg	gag	tat	tac	ttt	gct	tct	gat	gca	agt	gct	gtc	ata	gaa	cac	acc	864
Val	Glu	Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glu	His	Thr	
		275					280					285				
aat	cgc	gtc	atc	ttt	ctg	gaa	gat	gat	gat	gtt	gca	gca	gta	gtg	gat	912
Asn	Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp	
	290					295					300					
gga	cgt	ctt	tct	atc	cat	cga	att	aaa	cga	act	gca	gga	cat	cac	cat	960
Gly	Arg	Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His	
					310					315					320	
cac	cat	cac	gat	cac	ccc	gga	cga	gct	gtg	caa	aca	ctc	cag	atg	gaa	1008
His	His	His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu	
				325					330					335		
ctc	cag	cag	atc	atg	aag	ggc	aac	ttc	agt	tca	ttt	atg	cag	aag	gaa	1056
Leu	Gln	Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu	
				340				345					350			
ata	ttt	gag	cag	cca	gag	tct	gtc	gtg	aac	aca	atg	aga	gga	aga	gtc	1104
Ile	Phe	Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val	
		355					360					365				
aac	ttt	gat	gac	tat	act	gtg	aat	ttg	ggt	ggt	ttg	aag	gat	cac	ata	1152
Asn	Phe	Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile	
	370					375					380					
aag	gag	atc	cag	aga	tgc	cgg	cgt	ttg	att	ctt	att	gct	tgt	gga	aca	1200
Lys	Glu	Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	
					390					395					400	
agt	tac	cat	gct	ggc	gta	gca	aca	cgt	caa	gtt	ctt	gag	gag	ctg	act	1248
Ser	Tyr	His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	
				405					410					415		

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gag	ttg	cct	gtg	atg	gtg	gaa	cta	gca	agt	gac	ttc	ctg	gac	aga	aac	1296
Glu	Leu	Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	
			420					425					430			
aca	cca	gtc	ttt	cga	gat	gat	gtt	tgc	ttt	ttc	ctt	agt	caa	tca	ggg	1344
Thr	Pro	Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	
		435					440					445				
gag	aca	gca	gat	act	ttg	atg	ggg	ctt	cgt	tac	tgt	aag	gag	aga	gga	1392
Glu	Thr	Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	
	450					455					460					
gct	tta	act	gtg	ggg	atc	aca	aac	aca	gtt	ggc	agt	tcc	ata	tca	cgg	1440
Ala	Leu	Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	
465					470					475					480	
gag	aca	gat	tgt	gga	gtt	cat	att	aat	gct	ggg	cct	gag	att	ggg	gtg	1488
Glu	Thr	Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	
				485					490					495		
gcc	agt	aca	aag	gct	tat	acc	agc	cag	ttt	gta	tcc	ctt	gtg	atg	ttt	1536
Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe	
			500					505					510			
gcc	ctt	atg	atg	tgt	gat	gat	cgg	atc	tcc	atg	caa	gaa	aga	cgc	aaa	1584
Ala	Leu	Met	Met	Cys	Asp	Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys	
		515					520					525				
gag	atc	atg	ctt	gga	ttg	aaa	cgg	ctg	cct	gat	ttg	att	aag	gaa	gta	1632
Glu	Ile	Met	Leu	Gly	Leu	Lys	Arg	Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val	
	530					535					540					
ctg	agc	atg	gat	gac	gaa	att	cag	aaa	cta	gca	aca	gaa	ctt	tat	cat	1680
Leu	Ser	Met	Asp	Asp	Glu	Ile	Gln	Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	
545					550					555					560	
cag	aag	tca	gtt	ctg	ata	atg	gga	cga	ggc	tat	cat	tat	gct	act	tgt	1728
Gln	Lys	Ser	Val	Leu	Ile	Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	
				565					570					575		
ctt	gaa	ggg	gca	ctg	aaa	atc	aaa	gaa	att	act	tat	atg	cac	tct	gaa	1776
Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	
			580					585					590			
ggc	atc	ctt	gct	ggg	gaa	ttg	aaa	cat	ggc	cct	ctg	gct	ttg	gtg	gat	1824
Gly	Ile	Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	
		595					600					605				
aaa	ttg	atg	cct	gtg	atc	atg	atc	atc	atg	aga	gat	cac	act	tat	gcc	1872
Lys	Leu	Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	
	610					615					620					
aag	tgt	cag	aat	gct	ctt	cag	caa	gtg	gtt	gct	cgg	cag	ggg	cgg	cct	1920
Lys	Cys	Gln	Asn	Ala	Leu	Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	
625					630					635					640	
gtg	gta	att	tgt	gat	aag	gag	gat	act	gag	acc	att	aag	aac	aca	aaa	1968
Val	Val	Ile	Cys	Asp	Lys	Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	
				645					650					655		
aga	acg	atc	aag	gtg	ccc	cac	tca	gtg	gac	tgc	ttg	cag	ggc	att	ctc	2016
Arg	Thr	Ile	Lys	Val	Pro	His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	

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660					665					670						
agc	gtg	atc	cct	tta	cag	ttg	ctg	gct	ttc	cac	ctt	gct	gtg	ctg	aga	2064
Ser	Val	Ile	Pro	Leu	Gln	Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	
		675					680					685				
ggc	tat	gat	gtt	gat	ttc	cca	cgg	aat	ctt	gcc	aaa	tct	gtg	act	gta	2112
Gly	Tyr	Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	
	690					695					700					
gag	tga															2118
Glu																
705																

<210> 12
 <211> 705
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> (57)..(57)
 <223> 'xaa' in position 57 represents Thr or Ile

<220>
 <223> modified GFAT1Alt by an internal purification tag

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Arg	Glu	Ile	Leu	Glu	Thr	Leu	Ile	Lys	Gly	Leu	Gln	Arg	Leu	Glu	Tyr	
			20					25					30			
Arg	Gly	Tyr	Asp	Ser	Ala	Gly	Val	Gly	Phe	Asp	Gly	Gly	Asn	Asp	Lys	
		35					40					45				
Asp	Trp	Glu	Ala	Asn	Ala	Cys	Lys	Xaa	Gln	Leu	Ile	Lys	Lys	Lys	Gly	
	50					55					60					
Lys	Val	Lys	Ala	Leu	Asp	Glu	Glu	Val	His	Lys	Gln	Gln	Asp	Met	Asp	
65				70					75						80	
Leu	Asp	Ile	Glu	Phe	Asp	Val	His	Leu	Gly	Ile	Ala	His	Thr	Arg	Trp	
			85						90					95		
Ala	Thr	His	Gly	Glu	Pro	Ser	Pro	Val	Asn	Ser	His	Pro	Gln	Arg	Ser	
			100					105					110			
Asp	Lys	Asn	Asn	Glu	Phe	Ile	Val	Ile	His	Asn	Gly	Ile	Ile	Thr	Asn	
		115					120					125				
Tyr	Lys	Asp	Leu	Lys	Lys	Phe	Leu	Glu	Ser	Lys	Gly	Tyr	Asp	Phe	Glu	
	130					135					140					
Ser	Glu	Thr	Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Val	Lys	Tyr	Met	Tyr	
145					150				155						160	
Asp	Asn	Arg	Glu	Ser	Gln	Asp	Thr	Ser	Phe	Thr	Thr	Leu	Val	Glu	Arg	
			165						170					175		
Val	Ile	Gln	Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	

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180					185					190					
His	Phe	Pro	Gly	Gln	Ala	Val	Gly	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu
		195					200					205			
Ile	Gly	Val	Arg	Ser	Glu	His	Lys	Leu	Ser	Thr	Asp	His	Ile	Pro	Ile
	210					215					220				
Leu	Tyr	Arg	Thr	Ala	Arg	Thr	Gln	Ile	Gly	Ser	Lys	Phe	Thr	Arg	Trp
225					230					235					240
Gly	Ser	Gln	Gly	Glu	Arg	Gly	Lys	Asp	Lys	Lys	Gly	Ser	Cys	Asn	Leu
				245					250					255	
Ser	Arg	Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala
			260					265					270		
Val	Glu	Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glu	His	Thr
		275					280					285			
Asn	Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp
	290					295					300				
Gly	Arg	Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His
305					310					315					320
His	His	His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu
				325					330					335	
Leu	Gln	Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu
			340					345					350		
Ile	Phe	Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val
		355					360					365			
Asn	Phe	Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile
	370					375					380				
Lys	Glu	Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr
385					390					395					400
Ser	Tyr	His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr
				405					410					415	
Glu	Leu	Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn
			420					425					430		
Thr	Pro	Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly
		435					440					445			
Glu	Thr	Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly
	450					455					460				
Ala	Leu	Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg
465					470					475					480
Glu	Thr	Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val
				485					490					495	
Ala	Ser	Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe
			500					505					510		
Ala	Leu	Met	Met	Cys	Asp	Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys

GFAT-anglais

515 520 525
 Glu Ile Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val
 530 535 540
 Leu Ser Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His
 545 550 555 560
 Gln Lys Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys
 565 570 575
 Leu Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu
 580 585 590
 Gly Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp
 595 600 605
 Lys Leu Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala
 610 615 620
 Lys Cys Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro
 625 630 635 640
 Val Val Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys
 645 650 655
 Arg Thr Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu
 660 665 670
 Ser Val Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg
 675 680 685
 Gly Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val
 690 695 700
 Glu
 705

<210> 13
 <211> 608
 <212> PRT
 <213> Escherichia coli

<400> 13
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 Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala Gly
 20 25 30
 Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg Leu
 35 40 45
 Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu His
 50 55 60
 Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu Pro
 65 70 75 80
 Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val Val
 85 90 95

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His	Asn	Gly	Ile 100	Ile	Glu	Asn	His	Glu 105	Pro	Leu	Arg	Glu	Glu 110	Leu	Lys
Ala	Arg	Gly 115	Tyr	Thr	Phe	Val	Ser 120	Glu	Thr	Asp	Thr	Glu 125	Val	Ile	Ala
His	Leu 130	Val	Asn	Trp	Glu	Leu 135	Lys	Gln	Gly	Gly	Thr 140	Leu	Arg	Glu	Ala
Val 145	Leu	Arg	Ala	Ile	Pro 150	Gln	Leu	Arg	Gly	Ala 155	Tyr	Gly	Thr	Val	Ile 160
Met	Asp	Ser	Arg	His 165	Pro	Asp	Thr	Leu 170	Leu	Ala	Ala	Arg	Ser	Gly 175	Ser
Pro	Leu	Val	Ile 180	Gly	Leu	Gly	Met	Gly 185	Glu	Asn	Phe	Ile	Ala 190	Ser	Asp
Gln	Leu	Ala 195	Leu	Leu	Pro	Val	Thr 200	Arg	Arg	Phe	Ile	Phe 205	Leu	Glu	Glu
Gly	Asp 210	Ile	Ala	Glu	Ile	Thr 215	Arg	Arg	Ser	Val	Asn 220	Ile	Phe	Asp	Lys
Thr 225	Gly	Ala	Glu	Val	Lys 230	Arg	Gln	Asp	Ile	Glu 235	Ser	Asn	Leu	Gln	Tyr 240
Asp	Ala	Gly	Asp	Lys 245	Gly	Ile	Tyr	Arg	His 250	Tyr	Met	Gln	Lys	Glu 255	Ile
Tyr	Glu	Gln	Pro 260	Asn	Ala	Ile	Lys	Asn 265	Thr	Leu	Thr	Gly	Arg 270	Ile	Ser
His	Gly	Gln 275	Val	Asp	Leu	Ser	Glu 280	Leu	Gly	Pro	Asn	Ala 285	Asp	Glu	Leu
Leu	Ser 290	Lys	Val	Glu	His	Ile 295	Gln	Ile	Leu	Ala	Cys 300	Gly	Thr	Ser	Tyr
Asn 305	Ser	Gly	Met	Val	Ser 310	Arg	Tyr	Trp	Phe	Glu 315	Ser	Leu	Ala	Gly	Ile 320
Pro	Cys	Asp	Val	Glu 325	Ile	Ala	Ser	Glu	Phe 330	Arg	Tyr	Arg	Lys	Ser 335	Ala
Val	Arg	Arg	Asn 340	Ser	Leu	Met	Ile	Thr 345	Leu	Ser	Gln	Ser	Gly 350	Glu	Thr
Ala	Asp	Thr 355	Leu	Ala	Gly	Leu	Arg 360	Leu	Ser	Lys	Glu	Leu 365	Gly	Tyr	Leu
Gly	Ser 370	Leu	Ala	Ile	Cys	Asn 375	Val	Pro	Gly	Ser	Ser 380	Leu	Val	Arg	Glu
Ser 385	Asp	Leu	Ala	Leu	Met 390	Thr	Asn	Ala	Gly	Thr 395	Glu	Ile	Gly	Val	Ala 400
Ser	Thr	Lys	Ala	Phe 405	Thr	Thr	Gln	Leu	Thr 410	Val	Leu	Leu	Met	Leu 415	Val
Ala	Lys	Leu	Ser 420	Arg	Leu	Lys	Gly	Leu 425	Asp	Ala	Ser	Ile	Glu 430	His	Asp

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Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met Leu
435 440 445

Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp Lys
450 455 460

His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala Leu
465 470 475 480

Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Ala
485 490 495

Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Ala
500 505 510

Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu Lys
515 520 525

Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu Tyr
530 535 540

Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met His
545 550 555 560

Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe Tyr
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Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys Gly
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Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
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GFAT-anglais

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